

1/14

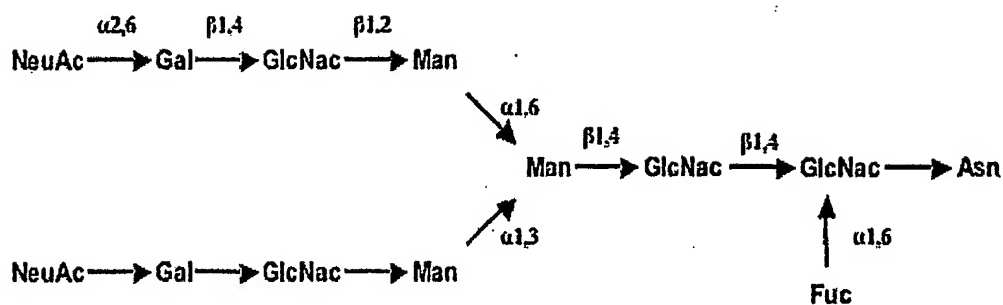


Figure 1

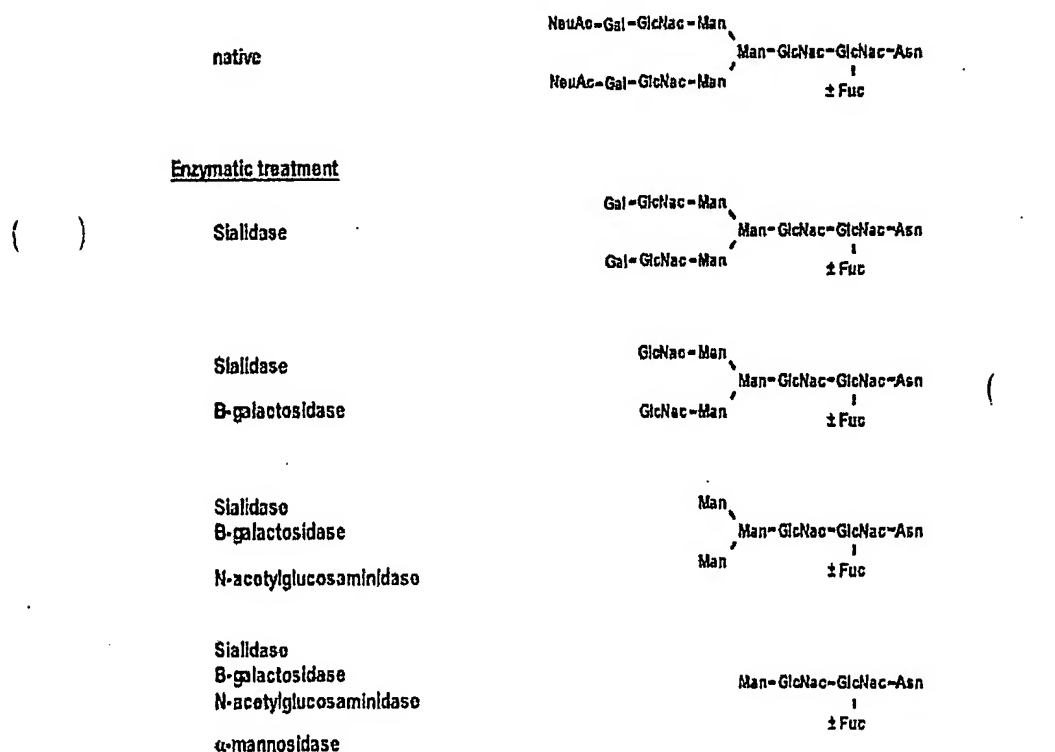


Figure 2

2/14

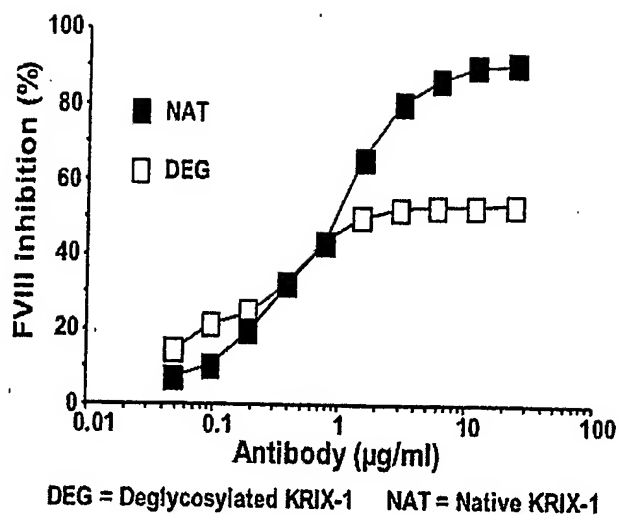


Figure 3

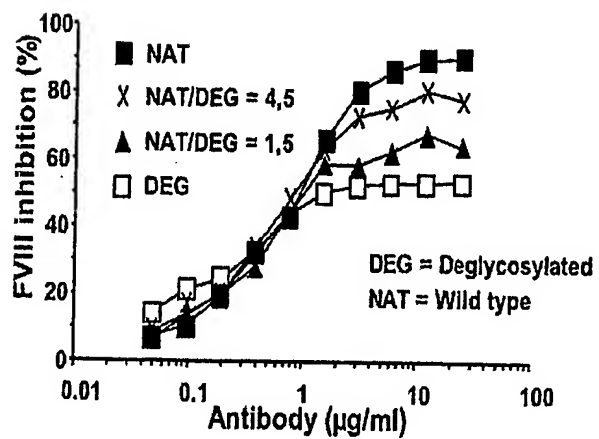


Figure 4

3/14

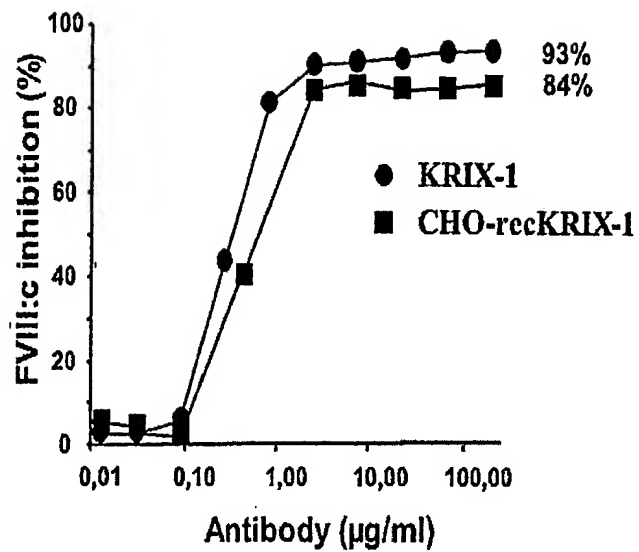


Figure 5

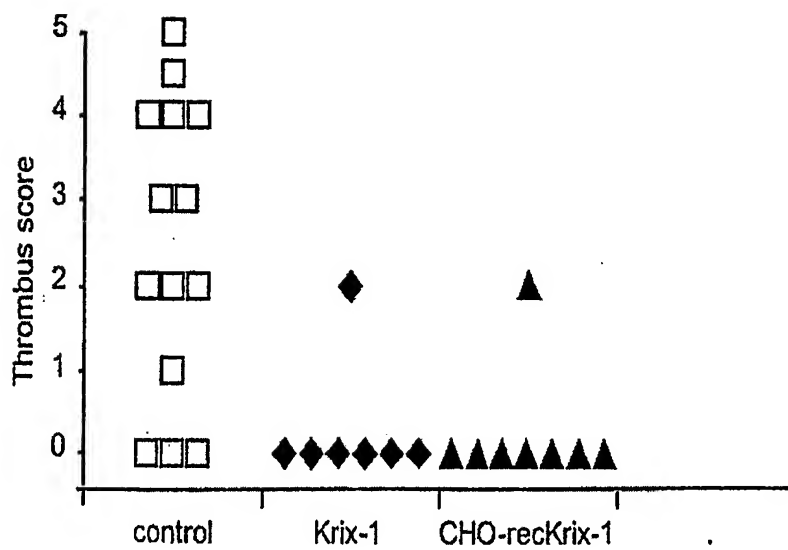


Figure 6

4/14

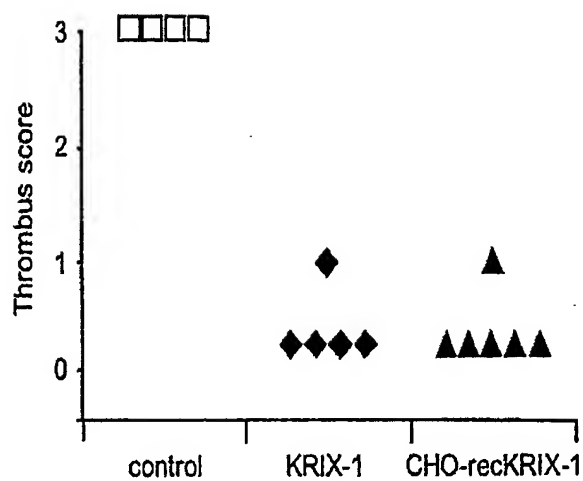


Figure 7

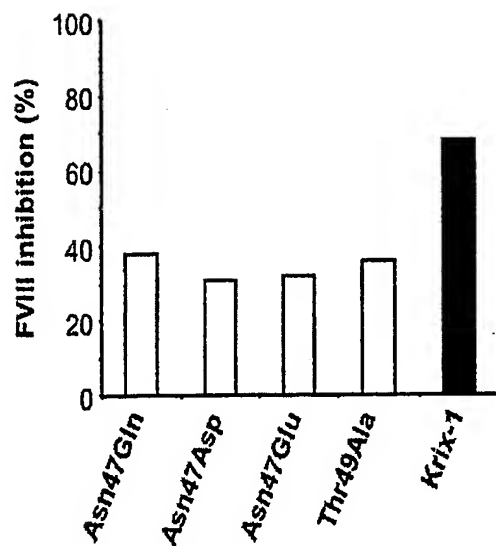


Figure 8

5/14

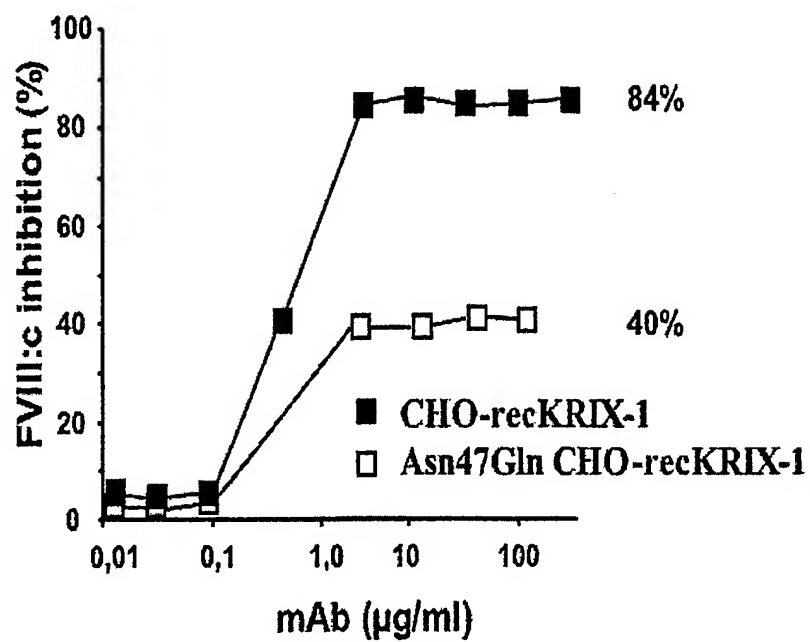


Figure 9

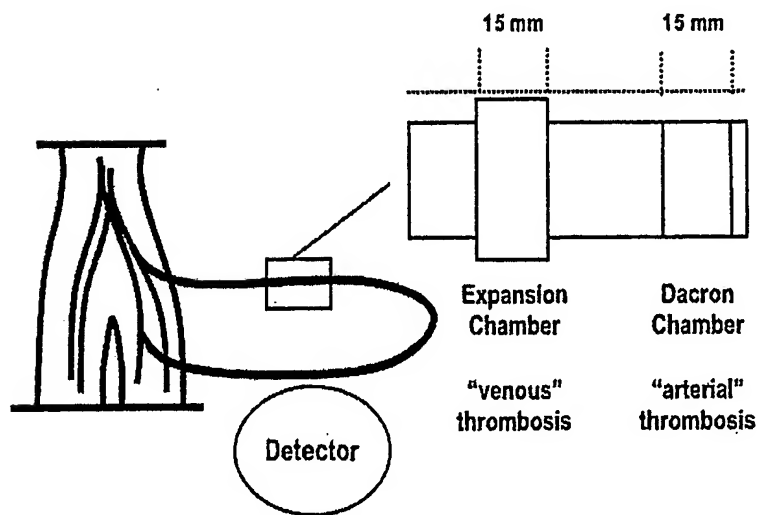


Figure 10

6/14

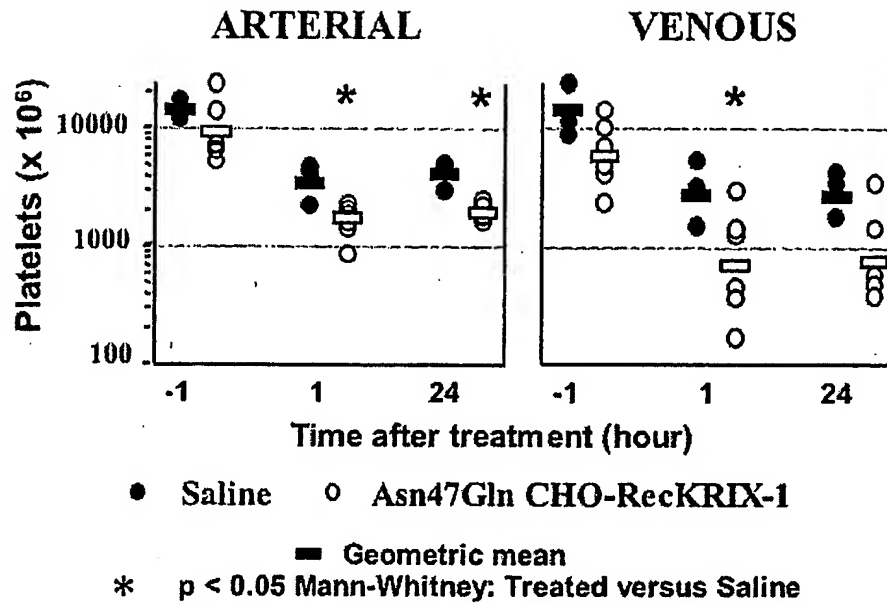


Figure 11

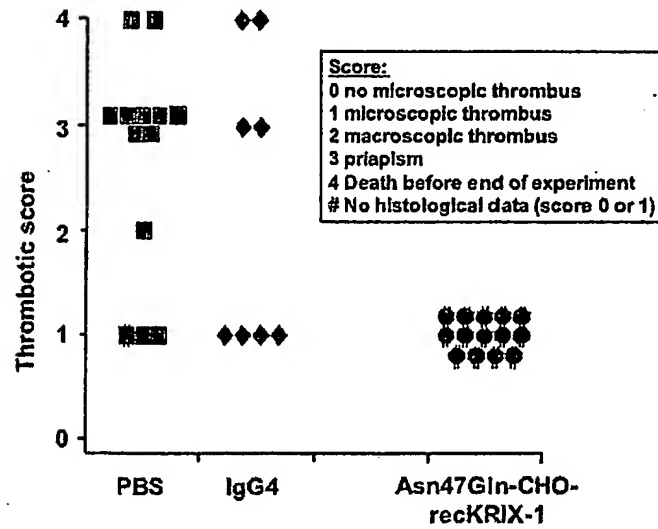


Figure 12

7/14

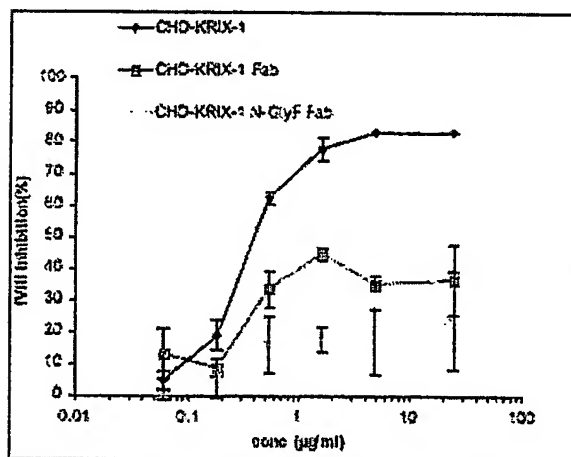
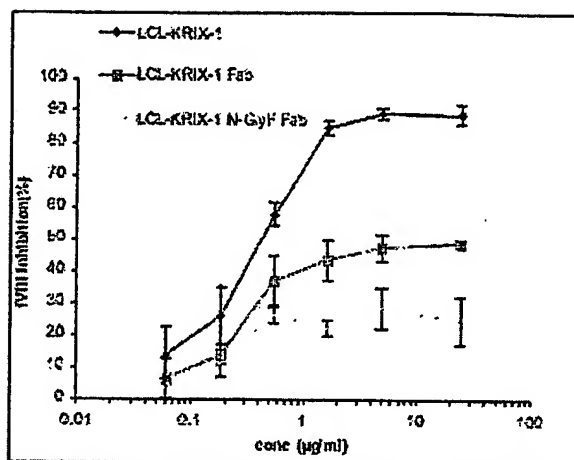


Figure 13

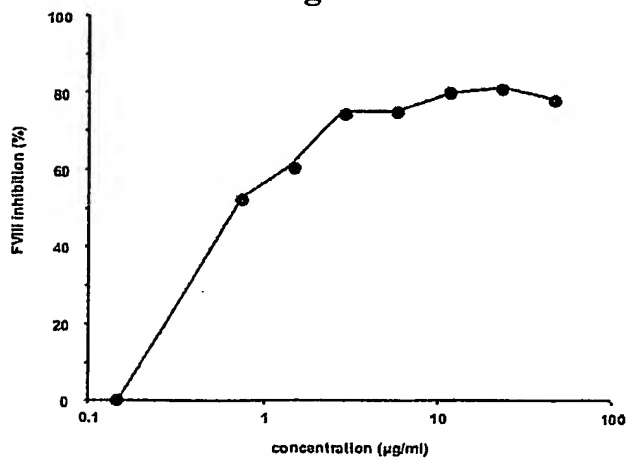


Figure 14

8/14

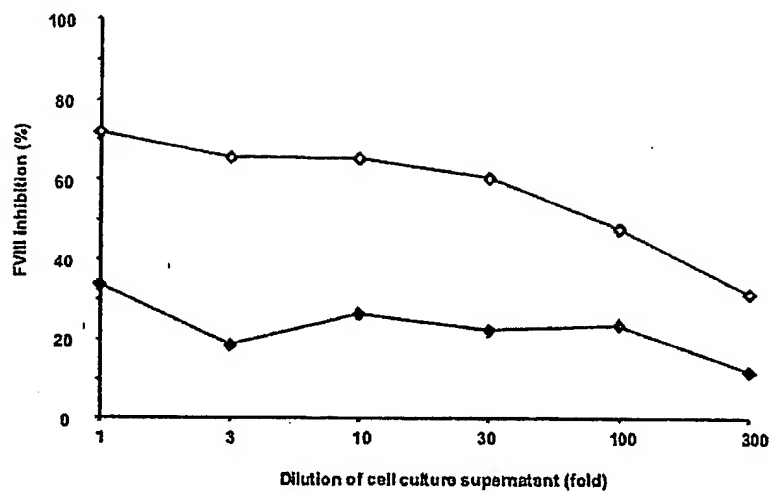


Figure 15

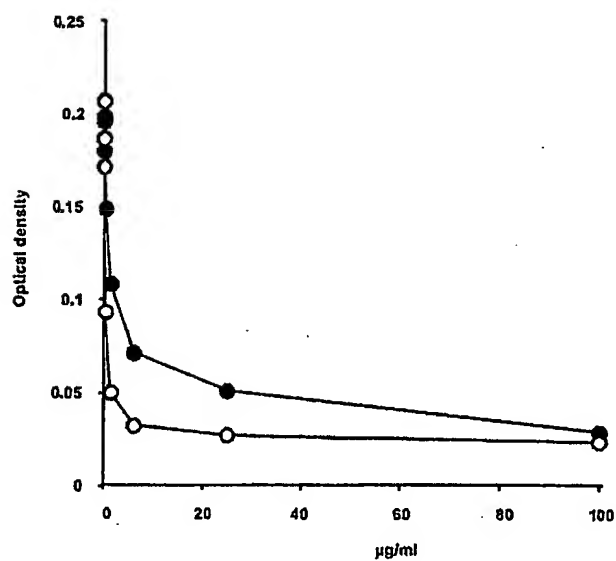


Figure 16

9/14

Krix-1 Variable heavy chain (SEQ ID NO: 1 and 2)

```

1/1                               31/11
ATG GAC TGG ACC TGG AGG ATC CTC TTC TTG GTG GCA GCA GCC ACA GGA GCC CAC TCC CAG
M  D  W  T  W  R  I  L  F  L  V  A  A  A  T  G  A  H  S  Q
<----- Leader peptide ----->

61/21                               91/31
GTG CAA CTG GTG CAA TCT GGG GCT GAG GTG AAG AAG CCT GGG GCC TCA GTG AAG GTC TCC
V  Q  L  V  Q  S  G  A  E  V  K  K  P  G  A  S  V  K  V  S

121/41                               47          49          151/51
TGC AAG ACC TCT GGA TAC AAC TTC ACC GGC TAC TCT GCT TCT GGA CAT ATC TTC ACC GCC
C  K  T  S  G  Y  N  F  T  G  Y  S  A  S  G  H  I  F  T  A
          *          *
<----- CDR1 ----->

181/61                               211/71
TAC TCT GTG CAC TGG GTG CGA CAG GCC CCT GGA CAA GGG CTT GAG TGG ATG GGA AGG ATC
Y  S  V  H  W  V  R  Q  A  P  G  Q  G  L  E  W  M  G  R  I
----->                               <----->

241/81                               271/91
AAC CCT AAC AGT GGT GCC ACA GAC TAT GCA CAT AAA TTT CAG GGC AGG GTC ACC ATG TCC
N  P  N  S  G  A  T  D  Y  A  H  K  F  Q  G  R  V  T  M  S
----- CDR2 ----->

301/101                               331/111
AGG GAC ACG TCC ATC AGC ACA GCC TAC ATG GAA CTG AGC AGG CTG ACA TCT GAC GAC ACG
R  D  T  S  I  S  T  A  Y  M  E  L  S  R  L  T  S  D  D  T

361/121                               391/131
GCC ATG TAT TAC TGT GCG AGA GCC GAC AAC TAT TTC GAT ATT GTG ACT GGC TAT ACT TCT
A  M  Y  Y  C  A  R  A  D  N  Y  F  D  I  V  T  G  Y  T  S
<----- CDR3 ----->

421/141                               451/151
CAT TAC TTT GAC TAC TGG GGC CGG GGA ACC CTG GTC ACC GTC TCC TCA GCC TCC ACC AAG
H  Y  F  D  Y  W  G  R  G  T  L  V  T  V  S  S  A  S  T  K
----->

481/161
GGC CCA TCG GTC TTC C
G  P  S  V  F

```

Figure 17

10/14

Krix-1 Variable light chain (SEQ ID NO: 3 and 4)

```

1/1                               31/11
ATG GAA ACC CCA GCT CAG CTT CTC TTC CTC CTG CTA CTC TGG CTC CCA GAT ACC ACC GGA
M  E  T  P  A  Q  L  L  F  L  L  L  L  W  L  P  D  T  T  G
<----- Leader ----->

61/21                             91/31
GAA ATT GTG TTG ACG CAG TCT CCA GGC ACC CTG TCT TTG TCT CCA GGG GAA AGA GCC ACC
E  I  V  L  T  Q  S  P  G  T  L  S  L  S  P  G  E  R  A  T

121/41                           151/51
CTC TCC TGC AGG GCC AGT CAG AGT GTT GCC AGC GCC TAC TTA GCC TGG TAC CAG CAA AAA
L  S  C  R  A  S  Q  S  V  A  S  A  Y  L  A  W  Y  Q  Q  K
<----- CDR1 ----->

181/61                           211/71
CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT GGT GCA TCC AGT AGG GCC ACC GAC ATC CCA
P  G  Q  A  P  R  L  L  I  Y  G  A  S  S  R  A  T  D  I  P
<----- CDR2 ----->

241/81                           271/91
CAC AGG TTC AGT GGC AGT GGG TCT GGG ACA GAC TTC ACT CTC ACC ATC AGC AGA CTG GAG
H  R  F  S  G  S  G  S  G  T  D  F  T  L  T  I  S  R  L  E

301/101                         331/111
CCT GAA GAT TTT GCA GTG TAC TAC TGT CAG CAA TAT GGT ACC TCA GCC TTA CTC ACT TTC
P  E  D  F  A  V  Y  Y  C  Q  Q  Y  G  T  S  A  L  L  T  F
<----- CDR3 ----->

361/121                         391/131
GGC GGA GGG ACC AAG GTG GAG ATC AAA CGA ACT GTG GCT GCA CCA TCT GTC TTC ATC TTC
G  G  G  T  K  V  E  I  K  R  T  V  A  A  P  S  V  F  I  F

421/141
CCG CCA TCT
( P ) P  S

```

Figure 17 (continued)

11/14

scFvLE2E9VLVH Q(His) (SEQ ID 25 and 26)

1/1 31/11
 atg gaa acc cca gcg cag ctt ctc ttc ctc ctg cta ctc tgg ctc cca gat acc acc gga
 M E T P A Q L L F L L L L W L P D T T G
 <----- Leader peptide ----->

61/21 91/31
 gaa att gtg ttg acg cag tct cca ggc acc ctg tct ttg tct cca ggg gaa aga gcc acc
 E I V L T Q S P G T L S L S P G E R A T
 <----->

121/41 151/51
 ctc tcc tgc agg gcc agt cag agt gtt gcc agc gcc tac tta gcc tgg tac cag caa aaa
 L S C R A S Q S V A S A Y L A W Y Q Q K

181/61 211/71
 cct ggc cag gct ccc agg ctc ctc atc tat ggt gca tcc agt agg gcc acc gac atc cca
 P G Q A P R L L I Y G A S S R A T D I P
 ----- VLJk -----

241/81 271/91
 cac agg ttc agt ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc aga ctg gag
 H R F S G S G S G T D F T L T I S R L E

301/101 331/111
 cot gaa gat ttt gca gtg tac tac tgt cag caa tat ggt acc tca gcc tta ctc act ttc
 P E D F A V Y Y C Q Q Y G T S A L L T F
 (-----)

361/121 391/131
 ggc gga ggg acc aag gtg gag atc aaa oga ggt gga ggc ggt tca ggc gga ggt ggc tot
 G G G T K V E I K R G G G G S G G G G S
 -----> <----- Linker ----->

421/141 451/151
 ggc ggt ggc gga tgc cag gta cag ctg gtg cag tot ggg gct gag gtg aag aag cct ggg
 G G G G S Q V Q L V Q S G A E V K K P G
 -----> <----->

481/161 511/171
 gcc tca gtg aag gtc tcc tgc aag acc tct gga tac caa ttc acc ggc tac tct gct tct
 A S V K V S C K T S G Y Q F T G Y S A S

Gln47 Thr49

541/181 571/191
 gga cat atc ttc acc gcc tac tct gtg cac tgg gtg cga cag gcc cct gga caa ggg ctt
 G H I F T A Y S V H W V R Q A P G Q G L

Figure 18

12/14

601/201

gag tgg atg gga agg atc aac cct aac agt ggt gcc aca gac tat gca cat aaa ttt cag
 E W M G R I N P N S G A T D Y A H K F Q

----- VHDJH -----

661/221

ggc agg gtc acc atg tcc agg gac acg tcc atc agc aca gcc tac atg gaa ctg agc agg
 G R V T M S R D T S I S T A Y M E L S R

721/241

ctg aca tct gac gac aca gcc atg tat tac tgt gcg aga gcc gac aac tat ttc gat att
 L T S D D T A M Y Y C A R A D N Y F D I

781/261

gtg act ggc tat act tct cat tac ttt gac tac tgg ggc cgg gga acc ctg gtc acc gtc
 V T G Y T S H Y F D Y W G R G T L V T V

841/281

tcc tca cat cat cat cat cat cat tga
 S S H H H H H H *

-----> <----- His(6) tag ----->

Figure 18 (continued)

13/14

RHD5 heavy chain variable region (SEQ ID NO: 29 and 30)

```

1/1                               31/11
ATG GAC TGG ACC TGG AGG TTC CTC TTT GTG GTG GCA GCA GCT GCA GGT GTC CAG TCC CAG
M D W T W R F L F V V A A A A G V Q S Q

<----- Leader peptide ----->
61/21                               91/31
GTG CAG CTG GTG CAG TCT GGG GCT GAG GTG AAG AAG CCC GGG TCG TCG GTG ATG GTC TCC
V Q L V Q S G A E V K K P G S S V M V S

121/41                               151/51
TGC AAG GCT TCT GGA GGC ACC TTC AGC AGC TTT GGT ATC AGC TGG GTG CGA CAG GCC CCT
C K A S G G T F S S F G I S W V R Q A P
<----- CDR1 ----->

181/61                               211/71
GGA CAA GGG CTT GAG TGG GTG GGA GGG ATC ATC CCT ATC TTT GGT ACA GCA AAC ACC GCA
G Q G L E W V G G I I P I F G T A N T A
<----- CDR2 ----->

241/81                               271/91
CGG AAC TTC CAG AAT AGA GTC ACC ATT ACC GCG GAC GAA TTC ACG AGC ACA GCC TAC ATA
R N F Q N R V T I T A D E F T S T A Y I
----->

301/101                               331/111
CGA CTG AGG AGC CTG AGA TCT GAA GAT ACG GCC GTG TAT TAC TGT GTC GGC GGT CGA GAT
R L R S L R S E D T A V Y Y C V G G R D
<----->

361/121                               391/131
GCC TAC AGC TTT GAT GGT TTT GAT GTC TGG GGC CAA GGG ACA ATG GTC ACC GTC TCT TCA
A Y S F D G F D V W G Q G T M V T V S S
----- CDR3 ----->

421/141
GCC TCC ACC AAG GGC CCA TCG GTC TTC CCC
A S T K G P S V F P
<-----constant region----->

```

Figure 19

14/14

RHD5 Light Chain Variable Region (SEQ ID NO: 31 And 32)

```

1/1                               31/11
ATG GCA TGG ATC CCT CTC TTC CTC GGC GTC CTT GTT TAC TGC ACA GGA TCC GTG GCC TCC
M  A  W  I  P  L  F  L  G  V  L  V  Y  C  T  G  S  V  A  S
<----- Leader peptide ----->

61/21                             91/31
TCT GGG CTG ACT CAG CCA CAC TCA GTG TCC GTG TCC CCA GGA CAG ACA GCC AAC ATC ACC
S  G  L  T  Q  P  H  S  V  S  V  S  P  G  Q  T  A  N  I  T
                               *      *

121/41                           151/51
TGC TCT AGA GAT AAG TTG GGT CAT AAA TTT GCT TCC TGG TAT CAA CAG AAG CCA GGC CAG
C  S  R  D  K  L  G  H  K  F  A  S  W  Y  Q  Q  K  P  G  Q
<----- CDR1 ----->

181/61                           211/71
TCC CCT GCT CTT CTC ATC TAT CAA GAC AGC AAG CGG CCC TCA GGG ATC CCT GAG CGA TTC
S  P  A  L  L  I  Y  Q  D  S  K  R  P  S  G  I  P  E  R  F
<----- CDR2 ----->

241/81                           271/91
TCT GGC TCC AAC TCT GGG AAC ACA GCC ACT CTG ACC ATC AGC GGG ACC CAG GCT ATG GAT
S  G  S  N  S  G  N  T  A  T  L  T  I  S  G  T  Q  A  M  D

301/101                          331/111
GAG GCT GAC TAT TAC TGT CAG GCG TGG GAC AAC ACC ACT GCC GTA TTC GGC GGA GGG ACC
E  A  D  Y  Y  C  Q  A  W  D  N  T  T  A  V  F  G  G  G  T
<----- CDR3 ----->
                               *      *

361/121                          391/131
AAG TTG ACA GTC CTA AGT CAG CCC AAG GCT GCC CCC TCG GTC ACT CTG TTC CCG CCC TCC
( K ) L  T  V  L  S  Q  P  K  A  A  P  S  V  T  L  F  P  P  S
<----- constant region ----->

```

Figure 19 (continued)